

SEQUENCE LISTING

<110> University of Utah Research Foundation

Bock, Susan C.

<120> Methods of Using High Affinity ATIII
Variants

<130> 21101.0054P1

<150> 60/618,746

<151> 2004-10-14

<150> 60/535,360

<151> 2004-01-09

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 1

Met	Tyr	Ser	Asn	Val	Ile	Gly	Thr	Val	Thr	Ser	Gly	Lys	Arg	Lys	Val
1				5					10					15	
Tyr	Leu	Leu	Ser	Leu	Leu	Leu	Ile	Gly	Phe	Trp	Asp	Cys	Val	Thr	Cys
			20					25					30		
His	Gly	Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro
		35					40					45			
Met	Asn	Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu
	50					55					60				
Asp	Glu	Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val
65					70					75				80	
Trp	Glu	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln
			85						90					95	
His	Leu	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro
			100					105					110		
Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn
			115				120					125			
Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser
	130					135						140			
Glu	Lys	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys
145					150					155					160
Arg	Leu	Tyr	Arg	Lys	Ala	Asn	Lys	Ser	Ser	Lys	Leu	Val	Ser	Ala	Asn
				165					170					175	
Arg	Leu	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp
			180					185					190		
Ile	Ser	Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys
		195					200					205			
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn
	210					215					220				

Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
 225 230 235 240
 Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
 245 250 255
 Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
 260 265 270
 Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
 275 280 285
 Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
 290 295 300
 Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
 305 310 315 320
 Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
 325 330 335
 Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
 340 345 350
 Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
 355 360 365
 Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
 370 375 380
 Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
 385 390 395 400
 His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
 405 410 415
 Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
 420 425 430
 Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
 435 440 445
 Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 450 455 460

<210> 2

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 Synthetic Construct

<400> 2

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atgtattcca	atgtgatagg	aactgtaacc	tctggaaaaa	ggaaggttta	tcttttgtcc	180
ttgctgctca	ttggcttctg	ggactgcgtg	acctgtcacg	ggagccctgt	ggacatctgc	240
acagccaagc	cgcgggacat	tcccatgaat	cccatgtgca	tttaccgctc	cccggagaag	300
aaggcaactg	aggatgaggg	ctcagaacag	aagatcccgg	aggccaccaa	ccggcgtgtc	360
tgggaactgt	ccaaggccaa	ttcccgtttt	gctaccactt	tctatcagca	cctggcagat	420
tccaagaatg	acaatgataa	cattttcctg	tcacccctga	gtatctccac	ggcttttgc	480
atgaccaagc	tgggtgcctg	taatgacacc	ctccagcaac	tgatggaggt	atttaagttt	540
gacaccatat	ctgagaaaac	atctgatcag	atccacttct	tctttgccaa	actgaactgc	600
cgactctatc	gaaaagccaa	caaatcctcc	aagtttagtat	cagccaatcg	cctttttgga	660
gacaaatccc	ttaccttcaa	tgagacctac	caggacatca	gtgagttggg	atatggagcc	720
aagctccagc	ccctggactt	caaggaaaat	gcagagcaat	ccagagcggc	catcaacaaa	780
tgggtgtcca	ataagaccga	aggccgaatc	accgatgtca	ttccctcgga	agccatcaat	840
gagctcactg	ttctgggtgct	ggttaacacc	atttacttca	agggcctgtg	gaagtcaaag	900
ttcagccctg	agaacacaag	gaaggaactg	ttctacaagg	ctgatggaga	gtcgtgttca	960
gcattctatga	tgtaccagga	aggcaagttc	cgttatcggc	gcgtggctga	aggcaccagg	1020
gtgcttgagt	tgcccttcaa	aggtgatgac	atcaccatgg	tctcatctt	gccaagcct	1080
gagaagagcc	tggccaaggt	ggagaaggaa	ctcacccccag	aggtgctgca	ggagtggctg	1140

gatgaattgg	aggagatgat	gctggtgggt	cacatgcccc	gcttccgcat	tgaggacggc	1200
ttcagtttga	aggagcagct	gcaagacatg	ggccttgctg	atctgttcag	ccctgaaaag	1260
tccaaactcc	caggtattgt	tgacagaaggc	cgagatgacc	tctatgtctc	agatgcattc	1320
cataaggcat	ttcttgaggt	aaatgaagaa	ggcagtgaag	cagctgcaag	taccgctgtt	1380
gtgattgctg	gccgttcgct	aaaccccaac	agggtgactt	tcaaggccaa	caggcccttc	1440
ctggttttta	taagagaagt	tcctctgaac	actattatct	tcatgggcag	agtagccaac	1500
ccttgtgtta	agtaaaatgt	tcttattctt	tgacacctct	cctatTTTTg	gtttgtgaac	1560
agaagtaaaa	ataaatacaa	actacttcca	tctcacatt			1599